WE CLAIM:

1.   A composition comprising a protein in crystalline form having unit cell dimensions, +/- 5%, of a=88.80Å b=88.80Å and c=174.99Å, α=β=γ=90 wherein at least a portion of the protein has at least 90% identity with residues 16-314 of SEQ. ID No. 1.

2.   A composition according to claim 1 wherein at least a portion of the protein has at least 95% identity with residues 16-314 of SEQ. ID No. 1.

3.   A composition according to claim 1 wherein the protein comprises consecutively of residues 16-314 of SEQ. ID No. 1.

4.   A composition according to claim 1 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5.   A composition according to claim 1 wherein the protein crystal has a crystal lattice in a P4$_1$22 space group.

6.   A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with residues 16-314 of SEQ. ID No. 1;

storing the crystallization volume under conditions suitable for crystal formation of the protein; and

forming a crystalline form of the protein having unit cell dimensions, +/- 5%, of a=88.80Å b=88.80Å and c=174.99Å, α=β=γ=90.

7.   A method according to claim 6 wherein at least a portion of the protein has at least 95% identity with residues 16-314 of SEQ. ID No. 1.

8.   A method according to claim 6 wherein at least a portion of the protein comprises consecutively of residues 16-314 of SEQ. ID No. 1.

9.   A method according to claim 6 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

10.   A method according to claim 6 wherein the protein crystal has a crystal lattice in a $P4_122$ space group.

11.   A method comprising:

diffracting a protein in crystalline form having unit cell dimensions, +/- 5%, of a=88.80Å b=88.80Å and c=174.99Å, $\alpha=\beta=\gamma=90$ wherein at least a portion of the protein has at least 90% identity with residues 16-314 of SEQ. ID No. 1; and

solving the structure of the protein from the diffraction pattern.

12.   A method according to claim 11 wherein at least a portion of the protein has at least 95% identity with residues 16-314 of SEQ. ID No. 1.

13.   A method according to claim 11 wherein at least a portion of the protein comprises consecutively of residues 16-314 of SEQ. ID No. 1.

14.   A method according to claim 11 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

15.   A method according to claim 11 wherein the protein crystal has a crystal lattice in a $P4_122$ space group.